# WEST Search History

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DATE: Tuesday, April 26, 2005

| Hide? | Set Name | Query | Hit Count |
|---|---|---|---|
| | | *DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ* | |
| ☐ | L1 | scatter$ diagram | 482 |
| ☐ | L2 | L1 same array | 14 |
| ☐ | L3 | L2 and gene expression | 2 |
| ☐ | L4 | L2 and (mRNA or expression sequence tag or EST) | 1 |
| ☐ | L5 | l1 and (high density near $array$) | 0 |
| ☐ | L6 | (high density near $array$) | 5166 |
| ☐ | L7 | l6 and l1 | 0 |
| ☐ | L8 | l1 and (microarray or array or microchip or biochip or chip) | 185 |
| ☐ | L9 | L8 and (gene expression or expression level or expression) | 67 |
| ☐ | L10 | L9 and (mRNA or EST or expression sequence tag) | 12 |
| ☐ | L11 | L10 and event | 8 |
| ☐ | L12 | L10 and (event or occurance) | 8 |
| ☐ | L13 | 10094407 | 2 |
| ☐ | L14 | 10042407 | 4 |
| ☐ | L15 | L14 and scatter diagram | 0 |
| ☐ | L16 | 10/042407 | 1 |
| ☐ | L17 | L16 and scatter diagram | 0 |
| ☐ | L18 | 5990078.pn. | 2 |
| ☐ | L19 | L16 and (database near search) | 1 |
| ☐ | L20 | L16 and (scatter near diagram) | 0 |
| ☐ | L21 | L16 and (scatter$ near diagram) | 0 |
| ☐ | L22 | L16 and (changes near expression) | 1 |
| ☐ | L23 | Scatter plot or scatter diagram | 1871 |
| ☐ | L24 | L23 and (microarray or microchip or chip or biochip or array) | 936 |
| ☐ | L25 | L24 and (expression level or gene expression or (expression near level)) | 340 |
| ☐ | L26 | L25 and (mRNA or est or express$ sequence tag) | 280 |
| ☐ | L27 | L26 and (response same (event or occurrance)) | 46 |
| ☐ | L28 | L27 and localiz$ | 38 |
| ☐ | L29 | L28 and (tissues or cells) | 38 |
| ☐ | L30 | L29 and (drug near development) | 14 |

| ☐ | L31 | L29 and (probe same hybridiz$) | 28 |
| ☐ | L32 | l27 and (screen$ near gene$) | 5 |

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| ☐ | L33 | screen$ near genes | 7073 |
| ☐ | L34 | screen$ near gene | 7073 |
| ☐ | L35 | (screen$ near gene) same (in situ hybridization) | 5 |
| ☐ | L36 | L34 same hybridization | 1089 |
| ☐ | L37 | L36 and (probe same (mRNA or express$ seqenc$ tag or EST)) | 593 |
| ☐ | L38 | L37 and (product near (gene expession)) | 0 |
| ☐ | L39 | L38 and (product same (gene expression)) | 0 |
| ☐ | L40 | L37 and (product same (gene expression)) | 281 |
| ☐ | L41 | L40 and (DNA chip or DNA microarray or microarray or microchip or chip) | 87 |
| ☐ | L42 | L41 and localization | 60 |
| ☐ | L43 | (probe same mRNA) same (in situ hybridization) | 835 |
| ☐ | L44 | L43 and (EST or exrpress$ sequence tag or mRNA) | 835 |
| ☐ | L45 | L44 and (Localization same mRNA) | 368 |
| ☐ | L46 | L45 and (different$ tissue or different cell) | 123 |
| ☐ | L47 | L46 and (DNA chip or DNA microarray or microarray or microchip or chip) | 62 |
| ☐ | L48 | (localization near MRNA) or (localization near (express$ sequence tag or EST)) | 408 |
| ☐ | L49 | L48 and (in situ hybridization) | 164 |
| ☐ | L50 | L49 and (probe near (specifically hybriz$) near mRNA) | 0 |
| ☐ | L51 | L49 and (probe near mRNA) | 38 |

*DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ*

| ☐ | L52 | screening near genes | 2187 |
| ☐ | L53 | L52 same in situ hybridization | 0 |
| ☐ | L54 | L52 and in situ hybridization | 114 |
| ☐ | L55 | L54 and (mRNA localization) | 0 |
| ☐ | L56 | L54 and (gene near unknown near function) | 1 |
| ☐ | L57 | L54 and (DNA chip or DNA microarray or microarray or microchip or chip) | 55 |

*DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ*

| ☐ | L58 | L54 and (gene near unknown near function) | 1 |
| ☐ | L59 | (screening near gene) and (gene near unknown near function) | 59 |
| ☐ | L60 | (screening near gene) same (gene near unknown near function) | 5 |
| ☐ | L61 | L60 and in situ hybridization | 0 |
| ☐ | L62 | L60 and hybridization | 1 |

| | | | |
|---|---|---|---:|
| ☐ | L63 | insitu hybridization and hybridization | 32 |
| ☐ | L64 | insitu hybridization and L59 | 0 |
| ☐ | L65 | L59 and (hybridization of FISH) | 0 |
| ☐ | L66 | L65 and hybridization | 0 |
| ☐ | L67 | L59 and hybridization | 53 |
| ☐ | L68 | L67 and epression level | 0 |
| ☐ | L69 | L67 and expression level | 34 |
| ☐ | L70 | L69 and (EST or express$ sequence tag) | 14 |
| ☐ | L71 | L70 and (increase$ or decrease$ or chang$ or modulat$) | 14 |
| ☐ | L72 | (Screening near gene) | 4855 |
| ☐ | L73 | L33 same (unknown near function) | 22 |
| ☐ | L74 | L73 and differential display | 2 |
| ☐ | L75 | L73 and hybridization | 11 |
| ☐ | L76 | L73 and (expressed sequence tag or EST) | 5 |
| ☐ | L77 | L76 and @pd > 20040823 | 1 |

END OF SEARCH HISTORY

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| | | *DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ* | |
| ☐ | L1 | 6342495.pn. | 2 |
| ☐ | L2 | L1 and (scatter near plot or scatter near diagram) | 0 |
| ☐ | L3 | insitu hybridization | 32 |
| ☐ | L4 | in situ hybridization | 6847 |
| ☐ | L5 | L4 and (high density near (array or microarray or microchip or chip or biochip)) | 330 |
| ☐ | L6 | L5 and (scatter near plot or scatter near diagram) | 4 |
| ☐ | L7 | l6 and (event or occurance) | 2 |
| ☐ | L8 | L7 and (EST or mRNA or expression sequence tag) | 2 |
| ☐ | L9 | l8 and (unknown or unannotat$) | 2 |
| ☐ | L10 | L9 and (before and after) | 2 |
| ☐ | L11 | 6342495.pn. and scatter | 0 |
| ☐ | L12 | 20030180740.pn. | 2 |
| ☐ | L13 | 6670138.pn. | 2 |
| ☐ | L14 | L13 and scatter | 0 |
| ☐ | L15 | L13 and scattered | 0 |
| ☐ | L16 | L13 and scatter$ | 1 |

END OF SEARCH HISTORY

Identifying genes specifically expressed in different cells
of a tissue type for producing cell-specific **gene
expression** profiles in a brain, comprises uses of a
polynucleotide **microarray**;
brain cell-associated **gene expression**
identification, DNA **array** and **expression**
profiling useful for drug screening and disease therapy

AUTHOR:              BONAVENTURE P; QUO J; LIU X; KAMME F; MEURERS B; LEYSEN J;
                     BAKKER M
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DOCUMENT TYPE:       Patent
LANGUAGE:            English
OTHER SOURCE:        WPI: 2002-340114 [37]
AN      2002-12864   BIOTECHDS

AB      DERWENT ABSTRACT:
     NOVELTY - A polynucleotide **microarray** method comprises at least
     one polynucleotide as fully defined in the specification, where the
     expression of polynucleotides is either increased or decreased in brain
     cells in a response to stress compared to normal brain cells, is new.
          DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the
     following: (1) screening a compound for effectiveness in altering
     expression of target polynucleotides fully defined in the specification,
     where the polynucleotide expression is either increased or decreased in
     brain cells in response to stress compared to normal brain cells; and (2)
     treating depression in a mammal comprises administering a compound
     identified in  (1).
          WIDER DISCLOSURE - Also disclosed are following: (1) **gene
     expression** profiles produced at a cellular **level** of
     multiple brain nuclei after Chronic Mild Stress (CMS) +/- chronic
     treatment with antidepressant imipramine; (2) a new putative
     antidepressant was tested to determine whether it has different in-vitro
     pharmacological properties, but similar behavioural effects of
     imipramine; and (3) potential new targets for drug discovery to identify
     compounds useful to treat depression and other neurological diseases
     and/or conditions.
          USE - The new method uses **microarray** technology to
     identify genes specifically expressed in different cells of a tissue
     type.  Hence, using this method, a catalogue of cell specific
     **gene expression** profiles or patterns that can be used
     to determine which genes are expressed and where in the adult rat brain
     or central nervous system is provided.  In addition, **gene
     expression** profiling of selected brain nuclei may help to
     elucidate the chronic mechanism of antidepressant action and may help to
     provide a treatment for depression (claimed).
          EXAMPLE - Total RNA extraction was carried out in a small volume
     (20microl/LCM sample) of denaturing buffer, containing 2-mercaptoethanol
     (10microl/ml) and polyinosine (300ng) were used.  The samples were
     incubated at 42degreesC for 10 minutes and rinsed twice with 500microl
     Rnase-free water and centrifuged.  A cDNA **microarray** containing
     2147 cDNA clones was used in this study.  All clones were printed as two
     independent spots on a given **chip**.  A contact pin
     **microarray** was used to spot the clones in duplicate.  Microarrays
     were hybridized and scanned with a confocal laser scanner.  Each
     **microarray** was normalized at the 75 percentile.  Intensity of
     each clone in the sample was determined as the average of the intensities
     on the two identical chips. The pair-wise similarity of **gene
     expression** profiles within a group of same samples was examined
     by **scatter-plot** and the correlation co-efficient was
     calculated.(89 pages)